IN THE CLAIMS:

Please cancel Claims 3 to 5 without prejudice or disclaimer of subject matter. Please amend Claims 2, 6, 7, and 20, and add new Claim 27, as shown below.

1. (Withdrawn) A DNA micro-array for detecting nucleic acid molecules having target base sequences in a sample comprising a substrate and nucleic acid probes having base sequences substantially complementary to the target base sequences immobilized on the substrate, wherein the array contains additional probes of one or several kinds selected from the following probes:

probes for internal standard nucleic acids of one or several kinds which hybridize with said internal standards and are added for quantitative evaluation of PCR of said nucleic acid molecules having the target base sequences;

probes for external standard nucleic acids of one or several kinds which hybridize with said external standards and are added for evaluation of accuracy of detection operation and for quantitative analysis of the amount of the probes having base sequences substantially complementary to the target base sequences;

and probes added for quantitative evaluation of the amount or density of said nucleic acid probes having base sequences substantially complementary to the target base sequences, which are immobilized by the same method as said nucleic acid probes.

2. (Currently Amended) A DNA micro-array for detecting nucleic acid molecules having target base sequences in a sample, said array comprising:

a substrate; and

nucleic acid probes ~~having~~ including base sequences ~~substantially~~ complementary to the target base sequences, the nucleic acid probes being immobilized on the substrate ~~immobilized on the substrate~~,

wherein the array contains ~~additional probes of one or several kinds selected from the following probes~~ at least two probes for external standard nucleic acids, said at least two probes having different sequences from each other and having sequences complementary to the external standard nucleic acids,

wherein said at least two probes are available for producing calibration curves for detecting an amount of the nucleic acid molecules having the target base sequences in the sample

~~probes for internal standard nucleic acids of one or several kinds which hybridize with said internal standards and are added for quantitative evaluation of PCR of said nucleic acid molecules having the target base sequences;~~

~~probes for external standard nucleic acids of one or several kinds which hybridize with said external standards and are added for evaluation of accuracy of detection operation and for quantitative analysis of the amount of the probes having base sequences substantially complementary to the target base sequences;~~

~~in which said internal and/or external standard nucleic acids are added in order to quantitatively determine a concentration of the target nucleic acid molecules in the sample~~.

3. to 5. (Cancelled)

6. (Currently Amended) The DNA micro-array according to claim 2, wherein ~~the internal standard~~ said at least two probes ~~and the external standard probes~~ are synthetic nucleic acids immobilized on the substrate.

7. (Currently Amended) The DNA micro-array according to claim 6, wherein the synthesized nucleic ~~acid has~~ acids each have a chain length of 15 to 75 bases.

8. (Withdrawn) A primer set for PCR of internal standard nucleic acids to be amplified together with target nucleic acids during an PCR of the nucleic acids having the target base sequences upon quantitatively detecting the nucleic acids having the target base sequences using a DNA micro-array, wherein

chain lengths of PCR products derived from the nucleic acids having the target base sequences are designed to be substantially equal to chain lengths of PCR products derived from the internal standard nucleic acids given by the primer set.

9. (Withdrawn) A kit for detecting a target base sequence, which contains a primer set for PCR of an internal standard nucleic acid to be amplified together with a target nucleic acid during PCR of the nucleic acid having the target base sequence upon quantitatively detecting the nucleic acid having the target base sequence using a DNA micro-array, comprising at least two of the primer sets according to claim 8 corresponding to different chain lengths when an amplified product derived from the nucleic acid having the target base sequence has at least two chain lengths.

10. (Withdrawn) The kit for detecting a target base sequence according to claim 9, wherein the primer sets include at least one primer set for an amplified product chain length of 200 bp or less, at least one primer set for an amplified product chain length of 200 to 500 bp, at least one primer set for an amplified product chain length of 500 to 2,000 bp and at least one primer set for an amplified product chain length of 2,000 bp or more.

11. (Withdrawn) A kit for detecting a target base sequence, which contains external standard nucleic acids to be added to a sample upon quantitatively detecting a target nucleic acid using a DNA micro-array, comprising at least two external standard nucleic acids which are synthesized nucleic acids labeled with a detectable marker.

12. (Withdrawn) The kit for detecting a target base sequence according to claim 11, wherein the marker comprises a fluorescent material, a radioactive material or a light emitting material.

13. (Withdrawn) A kit for detecting a target base sequence, which contains internal standard nucleic acids to be amplified together with a target nucleic acid during PCR of the nucleic acid having the target base sequence upon quantitatively detecting the nucleic acid having the target base sequence using a DNA micro-array, comprising at least two nucleic acids derived from microorganism or virus as internal standard nucleic acids having no homology with the target base sequence to be detected.

14. (Withdrawn) A DNA micro-array having the first set of nucleic acid probe dots including a plurality of target nucleic acids arranged in a matrix pattern on a substrate, further comprising the second set of nucleic acid probe dots for assay of amounts or a densities of the nucleic acids in said dots, which are formed by the same method as the formation of said first set of nucleic acid probe dots and arranged on part of a surface of the substrate having said second set of nucleic acid probe dots formed thereon and whose average nucleic acid density per dot is determined.

15. (Withdrawn) The DNA micro-array according to claim 14, further comprising a plurality of said second set of nucleic acid probe dots having different levels of average nucleic acid density with average nucleic acid density per dot determined as the nucleic acid probe dots for use as density standards.

16. (Withdrawn) The DNA micro-array according to claim 14, wherein the average nucleic acid density per dot of the nucleic acid probe dots having the determined average nucleic acid density per dot are determined by chemical analysis separately.

17. (Withdrawn) The DNA micro-array according to claim 16, wherein inductively coupled plasma mass spectrometry (to be abbreviated as ICP-MS hereinafter) is used for the chemical analysis for determining the average nucleic acid density per dot.

18. (Withdrawn) The DNA micro-array according to claim 14, wherein the nucleic acid probe comprises a single-stranded nucleic acid.

19. (Withdrawn) The DNA micro-array according to claim 14, wherein the nucleic acid probe including a single-stranded nucleic acid and a target nucleic acid introduced by hybridization of the nucleic acid probe are both existent on the substrate.

20. (Withdrawn-Currently Amended) An analyzing method for a DNA micro-array having nucleic acid probe dots including a plurality of nucleic acids arranged in a matrix pattern on a substrate, characterized in that:

on part of a surface of the substrate having said second set of nucleic acid probe dots formed thereon, nucleic acid probe dots whose average nucleic acid density per each dot has been determined are formed as density standards by the same method as the formation of said first set of nucleic acid probe dots, where the density standard nucleic acid probe dots are a plurality of nucleic acid probe dots having different levels of average nucleic acid densities, whose average nucleic acid density per each dot has been determined; and

a nucleic acid concentration of the first set of nucleic acid probe in each dot having an undetermined concentration arranged on the substrate is determined by the secondary ion mass spectrometry by using a calibration curve drawn based on signal intensities of secondary ions detected when secondary ion mass spectrometry is carried out on the plurality of said second set of nucleic acid probe dots having the different levels of average nucleic acid densities[[,]].

21. (Withdrawn) The analyzing method for a DNA micro-array according to claim 20, wherein time-of-flight type secondary ion mass spectrometry is used as the

secondary ion mass spectrometry.

22. (Withdrawn) The analyzing method for a DNA micro-array according to claim 21, wherein a secondary ion intensity detected by the secondary ion mass spectrometry is an integral intensity (count value) of specific secondary ions derived from the nucleic acid probes and released from a fixed area applied with primary ions when a dose of the primary ions is set to a fixed value of $1 \times 10^{14}/cm^2$ or less.

23. (Withdrawn) The analyzing method for a DNA micro-array according to claim 21, wherein a secondary ion intensity detected by the secondary ion mass spectrometry is an integral intensity (count value) of specific secondary ions derived from the nucleic acid probes and released from a fixed area applied with primary ions when the dose of the primary ions is set to a fixed value of $1 \times 10^{12}/cm^2$ or less.

24. (Withdrawn) The analyzing method for a DNA micro-array according to any one of claims 21 to 23, wherein the secondary ions detected by the secondary ion mass spectrometry include an anion obtained by eliminating one hydrogen atom from a base of one of adenine, thymine, guanine, cytosine, and uracil, or an anion selected from the group consisting of P^-, PO^-, PO_2^- and PO_3^- as the secondary ion derived from the nucleic acid probe.

25. (Withdrawn) The analyzing method for a DNA micro-array according to claim 21, further comprising displaying a detection result as an image which shows

secondary ion intensity two-dimensionally according to an application position of the primary ions, based on the secondary ion intensity detected by the secondary ion mass spectrometry.

26. (Withdrawn) A method of producing a DNA micro-array having nucleic acid probes arranged in a matrix pattern on a substrate, comprising, upon forming said second set of nucleic acid probe dots for use as density standards whose average nucleic acid density per each dot is determined on part of a surface of the substrate having said first nucleic acid probe dots formed thereon:

forming said first set of nucleic acid probe dots in the matrix pattern on the substrate; and

forming the second set of nucleic acid dots on the part of the surface of the substrate by the same method as the formation of said first set of nucleic acid probe dots, wherein the nucleic acid probe dots for use as the density standards whose average nucleic acid density per each dot is pre-determined.

27. (New) An analyzing method using the DNA micro-array according to claim 2, comprising the steps of:

hybridizing the external standard nucleic acids to said at least two probes, wherein the external standard nucleic acids have different concentrations, and wherein the external standard nucleic acids are labeled with a marker,

detecting amounts of the external standard nucleic acids hybridized to said at least two probes using the marker; and

making a calibration curve for detecting the nucleic acid molecules having the target base sequences on the basis of the detected amounts.